

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: ZENECA LIMITED
 (B) STREET: 15 STANHOPE GATE
 (C) CITY: LONDON
 (D) STATE: LONDON
 (E) COUNTRY: UNITED KINGDOM
 (F) POSTAL CODE (ZIP): W1Y 6LN

(ii) TITLE OF INVENTION: GENETIC CONTROL OF FRUIT RIPENING

(iii) NUMBER OF SEQUENCES: 57

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: GB PPD

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 785 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: U-U9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGCACGAGG AAAA	CTANG TGAGA	ANGAG ATAATCGTTG	ACCGAGGNAG	AGAATGGCGA	60
GCGAGAAGAG CAAA	ATCTCTG	ATCATCGGGG	GCACCGGGTA	CATCGGCAAG	120
TTGCGAGCGC CAGG	TGATAGT	AACCTACCT	TCGCTCTCGT	CCGGAGCACC	180
ACCGCCCCCG					
CCGGCCAACC CGA	GAGGCC	AAGCTCTGA	GCGACTTCCA	GGCCGCCGCG	240
GTCAACCTCG					
TCCAGGGGGA TAT	NATAAC	CACGAGAGTC	TGGTTAAGGC	GATCAAGCTG	300
GTGGATGTGG					
TCATCTCCCC CGT	CGGCTTC	GTGA	NCNTGA	NTGATCAGAC	360
CARAGATCATC	GACGCCATCN				
AANAAGCCGG AGG	ACACATC	AAGAGGTACC	TTCCATCGGA	GTTTGCGAAC	420
GACGTANACC					
GAAGCCATGC TGT	GAGCCA	GCAAAGTCTA	CCTTTGTCGT	CAAGCAACAA	480
ATCANAAGGG					
CTGTTGAGGC ATC	GCGGNTNC	CCTTACACCT	TTGTATCTTC	CAACTTTCTT	540
CGGTGGGTNT					
TTCTCTCCCG TAT	TATGACA	GCGAGGAGCC	ACTGGTCTCT	CCACGACAA	600
GGTTGTCATC					
TTAGGTTNACG GGA	ACNCAA	ACGATCTTCT	CNATGAANAC	GACTTCCGGA	660
CATCCCATT					
ANTCTTGGAT GAT	CCATAAC	CTGAACCAGG	TTCTATTCTT	TAAAACTCC	720
NCCACTTCTT					
NTCTCTTANG AN	CTNTTTC	CCTCTTGGGA	AAAAAATGTC	NNCTANACTT	780
CNAAAAGGGT					
TTANT					785

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CGGCACGAG	GAAGAAACT	AGGTGAGAA	GAGATAATCG	TTGACCGAGG	NAGAGATGG	60
CGAGCGAGAA	GAGCAAAATC	CTGATCATCG	GGGCACCGG	GTACATCGGC	AAGTTCATCG	120
TGTTTCGAG	CGCCAGGTTA	GGTAACCCTA	CCTTCGCTCT	CGTCCGAGC	ACCACGCGCC	180
CCGCCGGCCA	ACCCGAGAAG	GCCAAGCTCC	TGAGCGACTT	CCAGGCGGCC	GGCGTCAACC	240
TGTCACAGG	GGATATATAT	AACCACGAGA	GTCTGGTTAA	GGCGATCAAG	CTGGTGGATG	300
TGGTCATCTC	CCCCGTCGGC	TTGGGGCANC	TGANTGATCA	GACCAAGATC	ATCGACGCCA	360
TCAAGAAGC	CGGAGGACAC	ATCAAGAGGT	ACCTTCATC	GGAGTTTGGC	AACGACGTAN	420
ACCGAAGCCA	TGCTGTGGAG	CCAGCAAAGT	CGACCTTTGT	CGTCAAGCAA	CAAATCANAA	480
GGCTGTGTGA	GGCATCGGGT	ATCCCTTACA	CCTTTGTATC	TTCCAATCTC	TTGGGTGGGT	540
NTTTCCTCCC	GGTATTANGA	CAGGCAGGAG	CCACTGGTCC	TCCCACGGAC	AAGTTGTGCA	600
TCTTANGTGA	CGGGAACACA	AAAGCGATCT	TTCTCAATGA	ANACACATCC	GGACNTNCAC	660
NATTAAAGCA	GTGGATGATC	CGAAAACCTG	AACANGTICT	ATATCTGAAA	CCTTCGCGCA	720
CTCTTGICTC	ATNACAACCT	ATTTCCTCT	GGGAAAAAAA	NGTCNGCAA	ACTCCNAAAA	780
GGTCTACTTC	CCGGAAGAAA	AATCTGAANC	ANA			813

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGCACGAGGG	AAAAAGGAGA	TNATCGTTGA	CCGAGGAGAG	AATGGCGAGC	GAGAAGAGCA	60
AGATCCTGAT	CATCGGGGGC	ACGGGGTACA	TCGGCAAGTT	CATCGTGTTC	CGGACGCCCA	120
GTTTAGGTAA	CCCTACCTTC	GCTCTCGTCC	GGAGACCAAC	CGCCCCCGCC	GGCCAAACCCG	180

AGAAGGGCAA GCTCCTGAGC GACTTCCAGG CCGCGGGCGT CACCCCTGGTC CAGGGGGATA 240
TATATAACCA CNAGAGTCTG GTTAAGGCGA TCAAGCTGGT GGATGTGGTC ATCTCCCCCG 300
5 TOGGGTTCCG GCAGCTGAGT GATCAGACTA AGATCATCGA CGCCATCAAA GAAAGCCGGA 360
GGACACATCA AGAGGTACCT TCCATCGGGA GTTTGGCAAC GACGTANACC GAAGCCATGC 420
10 TGTGGAAGCC ANCAAAGTCG ACCTTTGTCTG TCAAGCAACA AATTANAAGG GCTGTGAGG 480
CATCGGGGAT CCCTTACACC TTTGTTATCT TCCAACCTCT TCGGTGGGTA TNCCTCCCC 540
GTATTGGGAC AGGCANGAAC CACTGGTCCT CCCACGGAC AAGGTTGTCT TCTTAGGTGA 600
15 ACGGGAACAC CAANGCGATC TTTCTCAATG AAGACAACAT CGGGACATNC CCNATTTAAC 660
CANTGGATGA TCCNANAACC TGAACAAGGT CTATTCTGTA AAACCTCNCC ATCTTCTTTT 720
TCTCATAACG AACCCNTTIN CCTCTT 746

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 795 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
(B) CLONE: U-0104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGCAGGAGGA AANGAGATAA TCGTTGACCG AGGCAGAGAA TGGCGAGCGA GAAGAGCAAA 60
ATCCTGATCA TCGGGGGCAC CGGTATACATC GGCAAGTTCA TCGTGTTCG GAGCGCCAGG 120
T TAGGTAACT CTACCTTCGC TCTCGTCCGG AGCACCACCG CCCCCGCGG CCAACCCGAG 180
45 AAGGCCAAGC TCCTGAGCGA CTTCAGGCCG GCCGGCGTCA CCTCTGTCCA GGGGGATATA 240
TATAACCACG AGAGTCTGCT TAAGGCGATC AAGCTGGTGG ATGTGGTCAT CTCCCCGCTC 300
50 GGGTTCCGGC AGCTGAGTGA TCAGACCAAG ATCATCGACG CCATCAAGA AGCCGGAGGA 360
CACATCAAGA GGTACCTTCC ATCGGGGAGTT TGGCAACGAC GTTANACCGA AGCCATGCTG 420
TGGAGCCAGC AAAGTCNACC TTTGTCTGTA AGCAACAAT CANAAGGGCT GTTGANGCAT 480
55 CGGGNTTCCC TTACACCTTI GTATCTTCCA ACTTCTTCGG TGGGTATTTC CTCCCGGTAT 540
TANGACAGCG AGGACCACCTG GTCCTCCCCA CNGACAAGGT TGTCTCTTA GGTGACNGGA 600
ACACAAAANC ATCTTTCTCN ATGAAGACAA CTCGGGACAT ACNCNATTAA AGCNGTGGAT 660
60 GATCCCAAAA CTGGAACAAG TTCCTATNTC TTGAAAACCT TCCCGCCCAA CCATCCTTTN 720
GTCTCCCNNT TAAACCNAACT CTCATTTCCT CCTCTCTGG GGAACAAAAA AAGGTCCGGC 780
65 NAANAACCTC CNAAA 795

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS: